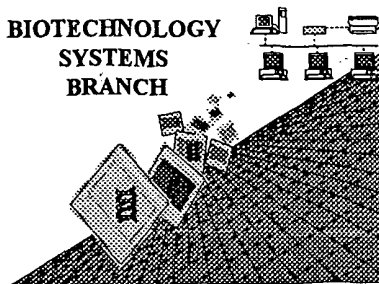BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/014,099*

Source: *OIPE*

Date Processed by STIC: *1/2/2002*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
      Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, r ther delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/014,099_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 01/02/2002
PATENT APPLICATION: US/10/014,099   TIME: 14:02:03

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Output Set: **N:\CRF3\01022002\J014099.raw**

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 5 <110> APPLICANT: KUEHN, Ralf
 7        FELDER, Susanne
 9        SCHWENK, Frieder
11        KUETER-LUKS, Birgit
13        FAUST, Nicole
17 <120> TITLE OF INVENTION: Modified Recombinase
21 <130> FILE REFERENCE: 012787wo/JH/ml
25 <140> CURRENT APPLICATION NUMBER: US/10/014,099
27 <141> CURRENT FILING DATE: 2001-12-11
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Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 01/02/2002
PATENT APPLICATION: US/10/014,099   TIME: 14:02:03

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Output Set: N:\CRF3\01022002\J014099.raw

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RAW SEQUENCE LISTING   DATE: 01/02/2002
PATENT APPLICATION: US/10/014,099   TIME: 14:02:03

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Output Set: N:\CRF3\01022002\J014099.raw

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RAW SEQUENCE LISTING   DATE: 01/02/2002
PATENT APPLICATION: US/10/014,099   TIME: 14:02:03

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515 <213> ORGANISM: Artificial Sequence
519 <220> FEATURE:
521 <223> OTHER INFORMATION: Description of Artificial Sequence: vector
523         pCMV-C31-Int(wt)
527 <400> SEQUENCE: 10
529 aaacagtccg atgtacgggc cagatatacg cgttgacatt gattattgac tagttattaa 60
531 tagtaatcaa ttacggggtc attagttcat agcccatata tggagttccg cgttacataa 120
533 cttacggtaa atggcccgcc tggctgaccg cccaacgacc cccgcccatt gacgtcaata 180
535 atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca atgggtggac 240
537 tatttacggt aaactgccca cttggcagta catcaagtgt atcatatgcc aagtacgccc 300
539 cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta 360
541 tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg 420
543 cggttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt 480
545 ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca 540
547 aaatgtcgta acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag 600
549 gtctatataa gcagagctct ctggctaact agagaaccca ctgcttactg gcttatcgaa 660
551 attaatacga ctcactatag ggagacccaa gctgactcta gacttaatta agcgttgggg 720
553 tgagtactcc ctctcaaaag cgggcatgac ttctgcgcta agattgtcag tttccaaaaa 780
555 cgaggaggat ttgatattca cctggcccgc ggtgatgcct ttgagggtgg ccgcgtccat 840
557 ctggtcagaa aagacaatct ttttgttgtc aagcttgagg tgtggcaggc ttgagatctg 900
559 gccatacact tgagtgacat tgacatccac tttgcctttc tctccacagg tgtccactcc 960
561 caggcggcc gcccgatatg acacaagggg ttgtgaccgg ggtggacacg tacgcgggtg 1020
563 cttacgaccg tcagtcgcgc gagcgcgaga attcgagcgc agcaagccca gcgacacagc 1080
565 gtagcgccaa cgaagacaag gcggccgacc ttcagcgcga agtcgagcgc gacggggcc 1140
567 ggttcaggtt cgtcgggcat ttcagcgaag cgccgggcac gtcggcgttc gggacggcgg 1200
569 agcgcccgga gttcgaacgc atcctgaacg aatgccgcgc cgggcggctc aacatgatca 1260
571 ttgtctatga cgtgtcgcgc ttctcgcgcc tgaaggtcat ggacgcgatt ccgattgtct 1320
573 cggaattgct cgccctgggc gtgacgattg tttccactca ggaaggcgtc ttccggcagg 1380
575 gaaacgtcat ggacctgatt cacctgatta tgcggctcga cgcgtcgcac aaagaatctt 1440
577 cgctgaagtc ggcgaagatt ctcgacacga agaaccttca gcgcgaattg ggcgggtacg 1500
```

<210> 19
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide 80d

<400> 19
```
ggtaccgagc tcggatcctc tagtaacggc cgccagtgtg ctggaattcg gcttcagcaa 60
ccaggctccc cagcaggcag aagtatgcaa agcatgcatc tcaattagtc agcaaccagg 120
tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca tctcaattag 180
tcagcaacca tagtcccgcc cctaactccg cccatcccgc ccctaactcc gcccagttcc 240
gcccattctc cgccccatgg ctgactaatt ttttttattt atgcagaggc cgaggccgcc 300
tcggcctagg aacagtcgac gacactgcag agacctactt cactaacaac cggtacagtt 360
cgtggaccag atgggtgagg tggagtacgc gcccggggag cccaaaggtt accccagttg 420
gggcactact cccgaaaacc gcttctggat ccataacttc gtatagcata cattatacga 480
agttataccg ggccaccatg gtcgcgagta gcttggcact ggggttgctt ttgcgggtc 540
gtgactggga aaaccctggc gttacccaac ttaatcgcct tgcagcacat ccccctttcg 600
ccagctggcg taatagcgaa gaggcccgca ccgatcgccc ttcccaacag ttgcgcagct 660
gaatggcgaa tggcgctttg cctggcttcc ggcaccagaa gcggtgccgg aaagctggct 720
ggagtgcgat cttcctgagg ccgatactgt cgtcaagccg aattctgcag atatccatca 780
cactggcggc cgctcgagca tgcatctaga gggccaattc gccctatagt gagtcgtatt 840
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

(MANDATORY)

insert <220> whenever <221>,<222>, or <223>

this is an amino acid present sequence

(see <212> response)

```
<210> 23
<211> 620
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: DNA sequence
      coding for fusion protein C31-Int(CNLS)

<400> 23
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```
L:25   M:270 C: Current Application Number differs, Replaced Application Number
L:27   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1861 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:1861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:1861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2811 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:6635 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:7051 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:7457 M:258 W: Mandatory Feature missing, <220> FEATURE:
```